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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 17, 2003, 18:55:45 ; Search time 2746 Seconds
(without alignments)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	286.4	27.5	1060	6	A21793	A21793 H. insolens
2	286.4	27.5	1060	6	A23635	A23635 H. insolens
3	286.4	27.5	1060	6	A23644	A23644 H. insolens
4	286.4	27.5	1060	6	A23953	A23953 Endoglucana
5	286.4	27.5	1060	6	A23957	A23957 Endoglucana
6	286.4	27.5	1060	6	A41658	A41658 Sequence 1
7	286.4	27.5	1060	6	A68060	A68060 Sequence 55
8	286.4	27.5	1060	6	AR059002	AR059002 Sequence
9	286.4	27.5	1060	6	AR072921	AR072921 Sequence
10	286.4	27.5	1060	6	AR163160	AR163160 Sequence
11	286.4	27.5	1060	6	BD010852	BD010852 Cellulase
12	286.4	27.5	1060	6	I13884	I13884 Sequence 1
13	286.4	27.5	1060	6	I21316	I21316 Sequence 1
14	286.4	27.5	1060	6	I57983	I57983 Sequence 1
15	286.4	27.4	1057	6	BD002248	BD002248 Cellulase
16	274.8	26.3	927	6	AR094307	AR094307 Sequence
17	273.4	26.2	894	6	AR094306	AR094306 Sequence
18	273.4	26.2	960	6	AR094305	AR094305 Sequence
19	271.8	26.1	922	6	A68070	A68070 Sequence 65
20	271.8	26.1	922	6	AR163167	AR163167 Sequence
21	268.2	25.7	922	6	A68078	A68078 Sequence 73
22	268.2	25.7	922	6	AR163171	AR163171 Sequence
23	260.2	24.9	1174	6	A92311	A92311 Sequence 1
24	260.2	24.9	1174	6	AR075389	AR075389 Sequence
25	260.2	24.9	1174	6	AR094310	AR094310 Sequence
26	257.4	24.7	919	6	A68072	A68072 Sequence 67
27	257.4	24.7	919	6	AR163168	AR163168 Sequence
28	246.2	23.6	1132	6	AR094315	AR094315 Sequence
29	240.2	23.0	913	6	AR094311	AR094311 Sequence
30	237.8	22.8	885	6	AR094316	AR094316 Sequence
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33	235.4	22.6	1473	6	A23637	A23637 F. oxysporu
34	235.4	22.6	1473	6	A23646	A23646 F. oxysporu
35	235.4	22.6	1473	6	A23955	A23955 Endoglucana
36	235.4	22.6	1473	6	A23959	A23959 Endoglucana
37	235.4	22.6	1473	6	A41660	A41660 Sequence 3
38	235.4	22.6	1473	6	AR072922	AR072922 Sequence
39	235.4	22.6	1473	6	BD002249	BD002249 Cellulase
40	235.4	22.6	1473	6	BD010853	BD010853 Cellulase
41	235.4	22.6	1473	6	I13885	I13885 Sequence 3
42	235.4	22.6	1473	6	I21317	I21317 Sequence 3
43	235.4	22.6	1473	6	I57984	I57984 Sequence 3
44	233	22.3	924	6	A68074	A68074 Sequence 69
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ALIGNMENTS

RESULT 1
LOCUS A21793 1060 bp mRNA linear PAT 20-SBP-1995
DEFINITION H.insolens mRNA for endonuclease component.
ACCESSION A21793
VERSION A21793.1 GI:1246872
KEYWORDS Humicola insolens.
SOURCE Humicola insolens
ORGANISM Humicola insolens
FEATURES
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	GGLPGORYGSISSNECDRFPDALKPGCYWRFDWFKNADNPSFRQVOCFAELVART				
	GCRNDGNFPVQI PPSSTSPVNPQTSTSTSTSSPPVQPTTSPGCTAERWAG				
	CGNGWSGCTTCVAGSTCTKINDYHOCL"				
BASE COUNT	190 a	377 c	288 g	205 t	
ORIGIN					
Query Match	27.5%;	Score 286.4;	DB 6;	Length 1060;	
Best Local Similarity	70.7%;	Pred. No. 2.5e-35;			
Matches	461;	Conservative	0;	Mismatches 166;	Indels 25; Gaps 5;
QY	381	CAGCGCTGTACGGGTGGCGCTAGCGGC-AACGGCGTCACTACCGCTACTGGGACTGCT	439		
Db	47	CGCGCTTCCGGTGTGGCGCTTGGCGCTGATGCGAGGTCCACCGCTACTGGGACTGCT	106		
QY	440	GCAAGCTTTCGTGCTGTCGTCGGCCGGCAAGGCTAAAGTCACTGCTGCTCAAGTCTGCA	499		
Db	107	GCAAGCTTTCGTGCTGTCGTCGGCCGGCAAGGCTCCCGTGAACAGGCTGCTTTTCTGCA	166		
QY	500	ACAAGAGCGGCTCAACCGCTCTTACGACTCCAAAGCCAGTCCCGCTGCAAA---CGGCG	556		
Db	167	AC---GCCAATTCAGCGTATCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT	223		
QY	557	GCAACTCTACATGTGCAACGACAGCCATGGGCTGTCAAGAGAGTGTCTCCAGTCAACCA	616		
Db	224	GTGTCGCTTACATCCCGTCTGTGTCGCGGCGACAGCCATGGGCTGTGAACAGGCTTCCG	283		
QY	617	GTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	676		
Db	284	GTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	343		
QY	677	AGCTCACTTCACTCCACAGCGTGTGCTGCGAAGAGATGCTGCTCCAGGTCAACCA	736		
Db	344	AGCTCACTTCACTCCCGTCTGTGTCGCGAAGAGATGCTGCTCCAGTCCACGCA	403		
QY	737	CTGCGGTGACCTTGGCAGCTCGACCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	796		
Db	404	CTGCGGTGATCTTGGCAGCA-----CCACTTCGATCTCAACATCCCGCGGCGG	454		
QY	797	CGCTGCGATCTCAACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	856		
Db	455	CGCTGCGATCTTCAACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	505		
QY	857	CGGCTACGGCGGATCAGTCCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	916		
Db	506	AGCGCTACGGCGGATCTCGTCCCGCAACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT	565		
QY	917	CGGCTGCAAGTGGCGCTTCAACTGGTTCAAGAACGCGGCTGCTGCTGCTGCTGCTGCTGCT	976		
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QY	977	AGGAGTCACTGCGGCGGAGATCAACCGCTAAGACCGGATGCTCGCGCA	1028		
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LOCUS	A23635		mRNA		
DEFINITION	H. insolens endoglucanase gene.				
ACCESSION	A23635				
VERSION	A23635.1				
KEYWORDS	Humicola insolens.				
SOURCE	Humicola insolens				
ORGANISM	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.				

BASE COUNT	190 a	377 c	288 g	205 t	
ORIGIN	CGGNGSWGCTTCVAGSTCTKINDWYHQCL*				
Query Match	27.5%	Score 286.4;	DB 6;	Length 1060;	
Best Local Similarity	70.7%	Prod. No. 2.5e-35;			
Matches 463; Conservative	0;	Mismatches 166;	Indels 25;	Gaps 5;	
QY	381	CAGCGCTGT	CAGCGGTGGCGCTACGGC-	AACGGCGTCA	TACCCGCTACTGGGACTGCT 439
Db	47	CCGCCCTGCCGGTGT	TGGCCCTTGGCCCT	GATGGCAGGTCCACCGCTACTGGGACTGCT 106	
QY	440	GCAAGGCTTCGTGCT	CGTGGCGCCGGCAAGGCTAACGTC	GAGTCGCGCTGTCAAAGCTCTGCA 499	
Db	107	GCAAGCCTTCGTGGGCT	TGGGCCAAGAAGGCTCCCGTGA	ACCAGCTGCTCTTTTCTGCA 166	
QY	500	ACAAGGACGGGTCA	CCGCTCTTAGCGACTTCAAACGCCCA	AGTCGGGTGCAA --- CGGCG 556	
Db	167	AC --- GCACACTTCC	CACCGTATCAGGACTTCGACGCG	CAAGTCGGGTGGAGCGGGCG 223	
QY	557	GCAACTCCTACATGT	GTGCAACGACAAACAGCGCATGGGCTGT	CAACGACAACTTGCTTTACG 616	

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RESULT 6
A41658 LOCUS linear PAT 05-MAR-1997
DEFINITION Sequence 1 from Patent EP0633311.
ACCESSION A41658
VERSION A41658.1 GI:2297284
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE Herbots,I.M. and Jansen,M.P.
AUTHORS Hydrophobic amines for cellulase stabilization in liquid detergent
TITLE Compositions containing anionic surfactant and cellulase
JOURNAL Patent : EP 0633311-A 1 11-JAN-1995;
COMMENT PROCTER & GAMBLE (US)
FEATURES Other publication CA 2165771 950105.
source Location/Qualifiers
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/db_xref="taxon:32644"
190 a 288 g 205 t
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	Best Local Similarity	70.7%	Pred. No. 2.5e-35			
	Matches 461	Conservative 0	Mismatches 166	Indels 25	Gaps 5	
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Db	47	CGCGCCCTGCGGGTGTTGGCCCTTGCCGCTGATGCGAGGTCCACCGCTACTGGGACTGCT	106			
QY	440	GCAAGCGTTCGTGCTCGTGGCCGGCAAGCTAACTCACTGCTCGCTGTCAAGTCTCGTCA	499			
Db	107	GCAAGCGCTTCGTGCGGCTGGGCCAAGAGCTCCCGTGAACAGACCTGTCTTTTCTCTGCA	166			
QY	500	ACAAGGACGGCGTCAACGCTTTTAGCGACTCCAAACGCCCAAGTCGGGTGCAA---CGGCG	556			
Db	167	AC---GCCAACTTCCAGCGTATCACGACTTCACAGCCCAAGTCGGGTGCGAGCGCGGCG	223			
QY	557	GCAACTCCTACATGTGCAACGCAACAGCGCATATGGGCTGTCAACAGCAACCTTGTCTTACG	616			

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797 GCGTCCGATCTTCAACGGATGCTCTGTCCTCAGTGGGCGGCTCCCAACGAGCGTGGGGCT 856
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857 GCGCTACGGCGGATCAGTCTCGCCAGCGATGCTCTGCTCTCCCGAGCGGCTCCAGG 916
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917 CCGCTGCAAGTGGGCTTCACTGTTCAGAGCGCGACCAACCGTCCATGACCTACA 976
566 CCGCTGCTACTGGCGCTTCACTGTTCAGAGCGCGACCAACCGTCCATGACCTACA 625
977 AGGAGTCACTGCTCCCAAGGAGATCACCGCTAAGACCGGATGCTCGCGCAA 1028
626 GTCAGTCCAGTGGCCCGGAGCTGCTCGCTCGACCGGATGCTCGCGCAA 677

RESULT 9
AR072921
LOCUS AR072921 1060 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 1 from patent US 5948672.
ACCESSION AR072921
VERSION AR072921.1 GI:9999684
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Rasmussen, G., Mikkelsen, J., Moslashedler, J., Schulein, M.,
Patkar, S., Anant, H., Hagen, F., Hjord, C., Mailand, and Hastrup, S.
TITLE Cellulase preparation comprising an endoglucanase enzyme
JOURNAL Patent: US 5948672-A 1 07-SEP-1999;
FEATURES Location/Qualifiers
source 1..1060
BASE_COUNT 190 a 377 c 288 g 205 t
ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;
Best Local Similarity 70.7%; Pred. No. 2.5e-35;
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;
381 CAGCGCTGTACGGGTGGCGCTAGCGGC-AACGGCGTCACTACCGCTACTGGGACTGCT 439
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797 GCGTCCGATCTTCAACGGATGCTCTGTCCTCAGTGGGCGGCTCCCAACGAGCGTGGGGCT 856
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977 AGGAGTCACTGCTCCCAAGGAGATCACCGCTAAGACCGGATGCTCGCGCAA 1028
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RESULT 10
AR163160
LOCUS AR163160 1060 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 55 from patent US 6270968.
ACCESSION AR163160
VERSION AR163160.1 GI:16233662
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Dalbo, O., Elashed, G. H., Sandal, T., Kauppinen, M., Sakari, and
Diderichsen, B., Shashedge.
TITLE Method of providing a hybrid polypeptide exhibiting an activity of
interest
JOURNAL Patent: US 6270968-A 55 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..1060
BASE_COUNT 190 a 377 c 288 g 205 t
ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;
Best Local Similarity 70.7%; Pred. No. 2.5e-35;
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;
381 CAGCGCTGTACGGGTGGCGCTAGCGGC-AACGGCGTCACTACCGCTACTGGGACTGCT 439
47 CCGCCCTGCGGTGTGGCGCTTGGCGCTGATGGAGGTCACCGCTACTGGGACTGCT 106
440 GCAAGCTTCTGCTCGTGGCGCGGCAAGGCTAAAGTCAAGTCTCGCTGTCAAGTCTCTGCA 499
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Db      224 GTGTCCGCTACTCTGTGCGCCGAGCAGACCCATATGGGCTGTGAACGACGACTTCGCGCTCG 283
Qy      617 GTTTCTGCTCGGCTGCCATTAAGCGGCTGGCGAGAGCCGCTGTGTCTGTCTCTGTCTTCG 676
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Qy      737 CTGCGGCTGACCTTGGCAGCTCGACCGGTGCCCACTTCCAGTCTCCAGATGCCCGGGGG 796
Db      404 CTGCGGCTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCCGGGGGGG 454
Qy      797 GCCTCGGCATCTTCAACGAGTGTCTGTCAGGTGGGGCGCTCCCAACGACGCGTGGGGCT 856
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Qy      857 CGCGCTACGCGGCGATCAGTCCCGCAGCACTGTCTGTCTCTCTCCCGAGCGGCTTCCAGG 916
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Qy      917 CGCGCTGCAAGTGGCGCTTCACTGTTTCAAGAGCGCGACACCGCTTCCAGCTTACA 976
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Qy      977 AGGAGGTCACTGCCCGCAGGAGATCACCGTAAAGCCGAGTCTCGCGCAA 1028
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RESULT 11

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LOCUS      BD010852                      1060 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Cellulase preparation containing endoglucanase.
ACCESSION  BD010852
VERSION    BD010852.1 GI:18639225
KEYWORDS   JP 2001057894-A/1.
SOURCE     Humicola insolens.
ORGANISM   Humicola insolens
REFERENCE  1 (bases 1 to 1060)
AUTHORS   Rasmussen,G., Mikkelsen,J.M., Schilein,M., Patkar,S.A., Hagen,F.,
           Miland,H.K. and Hallstopp,S.
TITLE      Cellulase preparation containing endoglucanase
JOURNAL    Patent: JP 2001057894-A 1 06-MAR-2001;
COMMENT    NOVO NORDISK AS
OS         Humicola insolens
PN         JP 2001057894-A/1
PD         06-MAR-2001
PF         06-JUL-2000 JP 2000205757
PR         09-MAY-1990 DK 1159/90, 22-APR-1991 DK 0736/91 PI
GURETE RASMUSSEN, JAN MOLLER MIKKJELSEN, MARTIN SCHILEIN, PI
SHAMKANT ANANT PATKAR, FRED HAGEN, HJOERT KARSTEN MILAND, PI SVEND
HALLSTOPP
PC         C12N15/09, C12D3/386, C12N11/15, C12N11/19, C12N9/24, D06M16/00// PC
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           C12R1:865),
PC         (C12N9/24, C12R1:885), (C12N9/24, C12R1:78), (C12N9/24, C12R1:69),
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BASE COUNT 190 a 377 c 288 g 205 t
ORIGIN
Query Match 27.5%; Score 286.4; DB 6; Length 1060;
Best Local Similarity 70.7%; Pred. No. 2.5e-35;
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;
Qy      381 CAGCGCTGTACGCGGTGGCGCTAGCGGC-AACGGCGTCACTACCCGCTACTGGGACTGCT 439
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Qy      500 ACAAGGAGCGGCTGACCGCTTTCAGGACTTCCAAACCCCGAGTCCGGCTGCAA---CGGCG 556
Db      167 AC---GC'AAC'TTCCAGCGTATCAGGACTTTCAGCGCAAGTCCGGCTGCGAGCGCGGCG 223
Qy      557 GCNACTCTTACATGTGCAAGCAGCAACAGGCATGGGCTGTCAACGACAACTTGTCTTACG 616
Db      224 GTGTCCGCTTACTGTGCGCGCAGCAGACCCCATATGGGCTGTGAACGACGACTTCGCGCTCG 283
Qy      617 GTTTCTGCTCGGCTGTGCATTTAGCGCGGTGGCGAGAGCGCTGTGTCTGTCTCTGTCTTCG 676
Db      284 GTTTTCTGCGCACTCTTATTTGCGGAGCAATGAGGGGGCTGTGTCTGTCTGTCTTACG 343
Qy      677 AGTCTACCTTCACTTCCAGCGTTCAGCGTTCGCGCAAGAGATGGTGTCTGTCTGTCTGTCTTAC 736
Db      344 AGTCTACCTTCACTTCCAGCGTTCGCTGTGCTGGCAAGAGATGGTGTCTGTCTGTCTGTCTTAC 403
Qy      737 CTGCGCGTGTACCTTGGCAGCTCGACCGGTGCCCACTTTCAGTCTCCAGATGCCCGGGGGG 796
Db      404 CTGCGCGTGTATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCCGGGGGGG 454
Qy      797 GCCTCGGCATCTTCAACGAGTGTCTGTCAGGTGGGGCGCTCCCAACGACGCGTGGGGCT 856
Db      455 GCCTCGGCATCTTCCAGGATGACTCCCGAGTTCGGGGCTGTGCCC-----GGCC 505
Qy      857 CGCGCTACGCGGCGATCAGTCCCGCAGCACTGTCTGTCTCTCTCCCGAGCGGCTTCCAGG 916
Db      506 AGCGCTACGCGGCGATCTCTGTCGCGCAACAGAGTCCGATCGGTTCCCGCAGCGGCTCAAG 565
Qy      917 CGCGCTGCAAGTGGCGCTTCACTGTTTCAAGAGCGCGACACCGCTTCCAGCTTACA 976
Db      566 CGCGCTGCTACTGGCGCTTCACTGTTTCAAGAGCGCGACATCCGAGCTTCAGCTTCC 625
Qy      977 AGGAGGTCACTGCCCGCAGGAGATCACCGTAAAGCCGAGTCTCGCGCAA 1028
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RESULT 12

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LOCUS      I13884                      1060 bp      DNA      linear      PAT 26-SEP-1995
DEFINITION Sequence 1 from patent US 5443750.
ACCESSION  I13884
VERSION    I13884.1 GI:996364
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1060)
AUTHORS   Convents,A., Busch,A. and Baek,A.C.
TITLE      Detergent compositions with high activity cellulase and softening
           clays
JOURNAL    Patent: US 5443750-A 1 22-AUG-1995;
FEATURES   Location/Qualifiers
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           /organism="unknown"
BASE COUNT 190 a 377 c 288 g 205 t

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ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;
Best Local Similarity 70.7%; Pred. No. 2.5e-35;
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;
QY 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439
DB 47 CGCGCTTGGCGGTGTGGCGCTTGGCGCTGATGGCAGGTCCACCGCTACTGGGACTGCT 106
QY 440 GCAAGGCTTGGCTGTGGCGCGGCAAGGCTAAGCTAGCTAGCTCGCTGTCAAGTCTCTGCA 499
DB 107 GCAAGGCTTGGCTGTGGCGCGGCAAGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT 166
QY 500 ACAAGGAGCGGTCAACCGCTTACGAGCTCCAGCGGCTCCAGCTCCGGCTGCAAA---CGGCG 556
DB 167 AC---GCCAACTTCAGCGTATACGAGCTTCAGCGGCTTGGCGCTTGGCGCTTGGCGGCG 223
QY 557 GCAACTCTTACATGTGCAAGCAACAGGCTATGGGCTGTCAACGCAAACTTGTCTTACG 616
DB 224 GTGTGGCTTACTCGTGGCGGACAGACCCATGGGCTGTGAACGAGCTTTCGGGCTCG 283
QY 617 GTTTCGCTGGCGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCT 676
DB 284 GTTTCGCTGGCGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCT 343
QY 677 AGCTCACCTTCACTCCAGGCTTGTGGCAAGAGATGGTGTCCAGGTCAACCAACA 736
DB 344 AGCTCACCTTCACTCCAGGCTTGTGGCAAGAGATGGTGTCCAGGTCAACCAACA 403
QY 737 CTGGCGGTGACTTGGCAGCTCGACCGGTGCGCACTTGGCTTCCAGTCCAGTCCGCGGCGG 796
DB 404 CTGGCGGTGACTTGGCAGCAAA-----CCACTTCGATCTCAACATCCCGCGGCGG 454
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DB 566 CGCGTCAAGTGGCGCTTCACTGGTTCAAGAGCGGCGGAGCTGTCTCCCTCCCGAGCGGCTCCAGG 625
QY 977 AGGAGTCACTGCGGCGGAGGATCAGCGCTTAAGACCGGATGCTCGCGCAA 1028
DB 626 GTGAGTCCAGTCCCGGAGCTGTCTCGCTCGACCGGATGCTCGCGCAA 677

RESULT 13
121316
LOCUS 121316 1060 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5520838.
ACCESSION 121316
VERSION 121316.1 GI:1601670
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1060)
AUTHORS Baek,A.C., Ceulemans,R.A. and Busch,A.
TITLE Compact detergent compositions with high activity cellulase
JOURNAL Patent: US 5520838-A 1 28-MAY-1996;
FEATURES Location/Qualifiers
source 1..1060
/organism="unknown"
BASE COUNT 190 a 377 c 288 g 205 t
ORIGIN
Query Match 27.5%; Score 286.4; DB 6; Length 1060;
Best Local Similarity 70.7%; Pred. No. 2.5e-35;
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;
QY 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439
DB 47 CGCGCTTGGCGGTGTGGCGCTTGGCGCTGATGGCAGGTCCACCGCTACTGGGACTGCT 106
QY 440 GCAAGGCTTGGCTGTGGCGCGGCAAGGCTAAGCTAGCTAGCTCGCTGTCAAGTCTCTGCA 499
DB 107 GCAAGGCTTGGCTGTGGCGCGGCAAGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT 166
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DB 284 GTTTCGCTGGCGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCTTACGAGCT 343
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QY 737 CTGGCGGTGACTTGGCAGCTCGACCGGTGCGCACTTGGCTTCCAGTCCAGTCCGCGGCGG 796
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QY 977 AGGAGTCACTGCGGCGGAGGATCAGCGCTTAAGACCGGATGCTCGCGCAA 1028
DB 626 GTGAGTCCAGTCCCGGAGCTGTCTCGCTCGACCGGATGCTCGCGCAA 677

RESULT 14
157983
LOCUS 157983 1060 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5610129.
ACCESSION 157983
VERSION 157983.1 GI:2483047
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1060)
AUTHORS McCorquodale,F. and Busch,A.
TITLE Dye transfer inhibiting compositions
JOURNAL Patent: US 5610129-A 1 11-MAR-1997;
FEATURES Location/Qualifiers
source 1..1060
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BASE COUNT 190 a 377 c 288 g 205 t
ORIGIN
Query Match 27.5%; Score 286.4; DB 6; Length 1060;
Best Local Similarity 70.7%; Pred. No. 2.5e-35;
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;
QY 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439

Db 47 CCGCCCTGCGGCTGTGGCCCTTGGCCCTGTAGTGGCAGGTCCACCCGCTACTGGGACTGCT 106
 Qy 440 GCAAGGCTTCGCTGCTGCTGGCCGCGCAAGCTTAACGTAGCTGCTGCTCAAGTCTGCA 499
 Db 107 GCAAGGCTTCGCTGCTGCTGGCCGCGCAAGGCTCCCGTGAACGAGCTGTCTTTCTGCA 166
 Qy 500 ACAAGGACGCGGTCAACCGCTCTTAGCGACTTCCAAACGCCAGTCCGGCTGCAA---CGGCG 556
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 Qy 677 AGCTCACTTCACTCCACAGCGTGTGCTGGCAAGAGATGCTGCTCCAGGTCACCAACA 736
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 Qy 857 CGGCTACGCGGCGATCAGCTCCCGCAGGAGTCTGCTGCTCCCTCCCGCAGCGGCTCCAGG 916
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 Db 566 CCGGCTGCTACTGCGGCTTTCGACTGTTCAAGAACCGCGACATCCGAGTTCAGCTTCC 625
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 Db 626 GTCAGGTCAAGTCCCGCAGGAGCTGCTGCTCGCACCGGATGCCCGCGAA 677

RESULT 15
 BD002248
 LOCUS 1057 bp DNA linear PAT 31-JAN-2002
 DEFINITION Cellulase preparation comprising endoglucanase.
 ACCESSION BD002248
 VERSION BD002248.1 GI:18630209
 KEYWORDS JP 2000217583-A/1.
 SOURCE Humicola insolens.
 ORGANISM Humicola insolens
 Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 Gurete,R., Moller,M.J., Martin,S. and Ananto,P.S.
 Cellulase preparation comprising endoglucanase
 Patent: JP 2000217583-A 1 08-AUG-2000;
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 OS Humicola insolens
 PN JP 2000217583-A/1
 PD 08-AUG-2000
 PR 22-DEC-1999 JP 1999365341
 PR 09-MAY-1990 DK 1159/90, 22-APR-1991 DK 0736/91 PI
 RASMUSSEN GURETE, MIKKJELSEN JAN MOLLER, SCHREIN MARTIN, PI PATKUL
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 Best Local Similarity 70.8%; Pred No. 2.9e-35;
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